

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 15 15:04:33 1999; MasPar time 3.81 Seconds

586.602 Million cell updates/sec
Tabular output not generated.

Title: >US-08-790-043B-2
Description: (1-256) from US08790043B.pep

Perfect Score:
Sequence: 1 MNLLENKTYVIMGJANKRSI. LSSGVGTGENIHYDGSFHAIK 256

Scoring table: PAM 150
Gap 11

Searched: 92929 seqs, 8738560 residues
Post-processing: Minimum Match 0% summaries
1:5_COMB 2:PCT9_COMB 3:backfiles

Database: a-issued
Statistics: Mean 30.516; Variance 165.768; scale 0.184

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	748	42.7	262	1	US-08-241- Sequence 9, Application 1.79e-47	
2	732	41.8	262	1	Sequence 8, Application 3.09e-46	
3	357	20.4	269	1	Sequence 6, Application 1.11e-17	
4	355	20.3	269	1	Sequence 7, Application 1.57e-17	
5	341	19.5	269	1	Sequence 4, Application 1.72e-16	
6	340	19.4	269	1	Sequence 5, Application 2.04e-16	
7	340	19.4	269	1	Sequence 14, Application 2.04e-16	
8	224	12.8	244	1	US-08-762- Sequence 3, Application 5.11e-08	
9	219	12.5	244	1	US-08-762- Sequence 4, Application 1.32e-07	
10	210	12.0	244	1	US-08-762- Sequence 1, Application 5.72e-07	
11	171	9.8	256	1	US-08-594- Sequence 7, Application 2.99e-04	
12	164	9.4	244	1	US-08-375- Sequence 13, Application 9.02e-04	
13	142	8.1	246	3	Patent No. 5229279-7	5229279-7
14	118	6.7	247	1	Sequence 13, Application 2.13e-02	
15	111	6.3	299	1	US-08-137- Sequence 6, Application 1.00e+00	
16	108	6.2	273	3	Patent No. 5512659-4	5512659-4
17	103	5.9	394	1	US-08-553- Sequence 1, Application 4.27e+00	
18	100	5.7	418	1	US-08-477- Sequence 3, Application 1.34e+01	
19	100	5.7	418	1	US-08-121- Sequence 3, Application 1.34e+01	
20	100	5.7	418	2	PCT-US93-0 Sequence 3, Application 1.34e+01	
21	100	5.7	764	1	PCT-US95-1 Sequence 4, Application 1.34e+01	
22	100	5.7	764	1	US-08-375- Sequence 4, Application 1.34e+01	
23	100	5.7	1089	2	PCT-US95-1 Sequence 2, Application 1.34e+01	

ALIGNMENTS

RESULT
ID US-08-241-766-9
XX STANDARD;
AC PRX;
XXXXXX DT

DE Sequence 9, Application US/08241766

XX Sequence 9, Application US/08241766

CC Patent No. 5686390

GENERAL INFORMATION:

APPLICANT: JACOBS, W. R.

APPLICANT: COLLINS, D. M.

APPLICANT: BANEREE, A.

APPLICANT: DELISE, G. W.

APPLICANT: WILSON, T. M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inHA AGE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER

STREET: 755 Page Mill Road

STATE: CA

CITY: Palo Alto

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/241,766

FILING DATE: 12-MAY-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MONROY, GLADYS H.

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 25237-20003.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 705141

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 amino acids

CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 SQ SEQUENCE 262 AA; 27864 MW; 329262 CN;

Query Match Score 748; DB 1; Length 262;
 Best Local Similarity 42.7%; Pred. No. 1.79e-4; Indels 3; Gaps 3;

Matches 111; Conservative 65; Mismatches 71; Indels 5; Gaps 5;

CC SEQUENCE 262 AA; 27761 MW; 329911 CN;

Db 4 LSGKRILYTGASKLSTAYGIAQAMHREGASLAFTYONDKIKGRYEEFAAGLG-SPIVL- 61
 QY 4 LENKTYVIMGANKRSTAFGAVKVLGALVFTVRKERSKELEKLLEBLNQPAHLY 63

Db 62 QCDVAEASIDTIFMAGKVPKDGFVHSIGFAPGDQLDDYNNATREOFKIAHDISS 121
 QY 64 QDQVSDEEVINGFEQIGKDVGNIDGYHSATAFANMEDLRGRFSET-SREFFLAQDISS 122

Db 122 YSFVAMAKACRSMLNPSSALLTLSYGAERAIPNPNMGMLAKASLEANVRYMANAMGPEG 181
 QY 123 YSLTIVAAHEAKKLMPPEGSIVATTYLGGEFAVONYNMGVAKASLEANVRYALDIDGPDN 182

Db 182 VVNAISAGPRTLNLASGKTRKMKLAHCTPIRRTVTEDVGSAAATLCSDSAGIS 241
 QY 183 VVNAISAGPRTLNLASGKTRKMKLAHCTPIRRTVTEDVGSAAATLCSDSAGIS 242

Db 242 GEVHVYDGGE 251
 QY 243 GENTHYDSGF 252

RESULT ID US-08-241-766-8 STANDARD; PRT; 262 AA.
 XX AC xxxxxx
 XX DT DT
 DE Sequence 8, Application US/08241766
 XX Sequence 8, Application US/08241766
 CC Patent No. 5686590
 CC GENERAL INFORMATION:
 CC APPLICANT: JACOBS, W. R.
 CC APPLICANT: COLLINS, D. M.
 CC APPLICANT: BANERJEE, A.
 CC APPLICANT: DELISLE, G. W.
 CC APPLICANT: WILSON, T. M.
 CC TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: MORRISON & FOERSTER
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/241,766
 CC FILING DATE: 12-MAY-1994
 CC CLASSIFICATION: 514
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: MORNOY, GLADYS H.
 CC REGISTRATION NUMBER: 32,430
 CC REFERENCE/DOCKET NUMBER: 25237-20003 .20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 833-5600
 CC TELEFAX: (415) 494-0792

CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 8:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 262 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 SQ SEQUENCE 262 AA; 27761 MW; 329911 CN;

Query Match Score 732; DB 1; Length 262;
 Best Local Similarity 43.8%; Pred. No. 3.09e-46;
 Mismatches 71; Indels 5; Gaps 5;

Db 4 LSGRILYVGASKLSTAYGIAQAMHREGASLAFTYONDKIKGRYEEFAAGLGSSIV-L- 61
 QY 4 LENKTYVIMGANKRSTAFGAVKVLGALVFTVRKERSKELEKLLEBLNQPAHLY 63

Db 62 PCDVADASIDTAMFABL-G-NWPKFDGFVHSIGFAPGDQLDDYNNATREOFKIAHDIS 120
 QY 64 QIDVQSEEVINGFEOIGKDV-GNLDGVYHTIAFANMDLRGRFSET-SREFFLAQDIS 121

Db 121 SYSFVAMAKACRTMINSGLASSLTSYGAERAIPNPNMGMLAKASLEANVRYMANAMGPE 180
 QY 122 SYSLTIVAAHEAKKLMPPEGSIVATTYLGGEFAVONYNMGVAKASLEANVRYALDIDGP 181

Db 181 GVRVNAISAGPRTLNLASGKTRKMKLAHCTPIRRTVTEDVGSAAATLCSDSAGI 240
 QY 182 NIRVNAISAGPRTLNLASGKTRKMKLAHCTPIRRTVTEDVGSAAATLCSDSAGI 240
 QY 182 NIRVNAISAGPRTLNLASGKTRKMKLAHCTPIRRTVTEDVGSAAATLCSDSAGI 240
 Db 241 SGEVHVYDGGE 251
 QY 242 TGENDHDSGF 252

RESULT ID US-08-241-766-6 STANDARD; PRT; 269 AA.
 XX AC xxxxxx
 XX DT DT
 DE Sequence 6, Application US/08241766
 XX Sequence 6, Application US/08241766
 CC Patent No. 5686590
 CC GENERAL INFORMATION:
 CC APPLICANT: BANERJEE, A.
 CC APPLICANT: DELISLE, G. W.
 CC APPLICANT: WILSON, T. M.
 CC APPLICANT: COLLINS, D. M.
 CC APPLICANT: MORRISON, & FOERSTER
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/241,766
 CC FILING DATE: 12-MAY-1994
 CC CLASSIFICATION: 514
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: MONROY, GLADYS H.
 CC REGISTRATION NUMBER: 32,430
 CC REFERENCE/DOCKET NUMBER: 25237-20003 .20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 833-5600
 CC TELEFAX: (415) 494-0792

REFERENCE/DOCKET NUMBER: 25237-20003.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141
 INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE 269 AA; 28527 MW; 364311 CN;

Query Match 4 20.4%; Score 357; DB 1; Length 269;
 Best Local Similarity 35.4%; Pred. No. 1.11e-17;
 Matches 93; Conservative 59; Mismatches 92; Indels 14;

Db 5 LEGKRILVINGITISSIAFHIAKYAQEAGAEVLIT-GFDRL-KLVKRAIDLRLPKP-APLL 61

Qy 4 LENKTYVINGIANKRSIAFGVAKYDOLGAKLYFTYRKERSRREKLUOLNQPEAHY 63

Db 62 ELDVQEHHHSTLADRITAEIGEKGKIDGVVHAIGFMPMSGMGINPPFDAPYEDVSKGH 121

Qy 64 QIDYQSDEEVINGEQIGKDVG- N-IDGYWHSSTAFAMMDL-RGRFSTTSREGFLAQD 119

Db 122 ISAYSYASLAKAVLPIMPGGTGMDF-DPTRAMPAYNWMVYAKSALESVNRFVAREAG 180

Qy 120 ISSSLTIVAHHEAKKLMPGGSIATVYGGFAYQNTNVYAKASLEANVYXALDIG 179

Db 181 KVGYRSNLVYAGPIRTLMSAIVGALGDEAQGOMQMLLEGWDORAPLGWNMKDPTPVAK 240

Qy 180 PDNTRVNTSAGPIRTLSKAG-VGG-F-N-T----ILKEI-EERAPLKRNV-DQVEYGK 228

Db 241 TVCALLSDWPAITGTVIADGG 263

Qy 229 TAAYLSDLSGVTGENIHVDSG 251

RESULT 4
 ID US-08-241-766-7 STANDARD; PRT; 269 AA.
 XX
 AC
 XXXXXX

RESULT 5
 ID US-08-241-766-4 STANDARD; PRT; 269 AA.

XX
 AC
 XXXXXX

Sequence 7, Application US/08241766

CC Sequence 7, Application US/08241766

CC General Information:

CC APPLICANT: JACOBS, W. R.

CC APPLICANT: COLLINS, D. M.

CC APPLICANT: DELISLE, G. W.

CC APPLICANT: WILSON, T. M.

CC TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORRISON & FOERSTER

CC STREET: 755 Page Mill Road

CC CITY: Palo Alto

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 94304-1018

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/241,766

CC FILING DATE: 12-MAY-1994

CC CLASSIFICATION: 514

CC ATTORNEY/AGENT INFORMATION:

CC NAME: MONROY, GLADYS H.

CC REGISTRATION NUMBER: 32,430

CC REFERENCE/DOCKET NUMBER: 25237-20003.20

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600

CC TELEFAX: (415) 494-0792

CC TELEX: 706141

CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC SEQUENCE 269 AA; 28511 MW; 362901 CN;

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

CC Query Match 20.3%; Score 355; DB 1; Length 269;

CC Best Local Similarity 35.0%; Pred. No. 1.57e-17;

CC Matches 92;保守性 60; Mismatches 92; Indels 19; Gaps 14;

CC Sequence 269 AA.

CC Sequence Characteristics:

CC LENGTH: 269 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC Sequence 269 AA.

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/241,766
 FILING DATE: 12 MAY 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, GLADYS H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 25237-200003.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706411
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE: 269 AA; 38514 MW; 350722 CN;

Query Match 19.5%; Score 341; DB 1; Length 269;
 Best Local Similarity 33.5%; Pred. No. 1.72e-16; Gaps 14;
 Matches 89; Conservative 65; Mismatches 93; Indels 19; Gaps 14;

Db 5 LDGKRILVSGITDSSTIAFHARVAQEGQAQLVT-GFDRLRL-IQRITDRL-PAKAPLL 61
 QY 4 LENTKVIMGIAKRSIAFGVAKVLQDQAKLVFLTYRKERSKELEKQUNQEPAHL 63

Db 62 ELDVQNEEHLASLAGRTYEAGNKLGDGVHSIGFMQTGNGINPFFADYVSKGIH 121
 QY 64 QIDVQSDEEVINGEQIIGKDVG--N-IDGVYHSIAFANMEDL-RGRSESETREGFLAQD 119

Db 122 ISAVSYASMAKALLPIMPNGGSTVGMDF-DPSRAMPAYNMVAKSALESYNRFAREAG 180
 QY 120 ISSYSLTIVAAEKKLMPFEGGSIVATIYLGGGEFAYQNYNMVGAKASLEANKYKLALDG 179

Db 181 KGYVRSLNLVAGPIRTLAMSATVGGAGBEAGAOIQLEGGDQRAPIGWNNKDAIPVAK 240
 QY 180 PDNTRVNAISAGPRTLSAKG-VGG-F-NT---I-LKEI-EERAPLKRVN-DOVEVK 228

Db 241 TYCALSDDWLPAATGDLIYADGGAHT 266
 QY 229 TAAYLLSDLSGVTGENIHVDSGFHA 254

RESULT 6 ID US-08-241-766-5 STANDARD: PRT; 269 AA.
 XX AC xxxxxx
 DT DE XX
 XX DE XX
 Sequence 5, Application US/08241766
 CC Pat. No. 5686590
 GENERAL INFORMATION:
 APPLICANT: JACOBS, W. R.
 APPLICANT: COLLINS, D. M.
 APPLICANT: BANNERETTE, A.
 APPLICANT: DELISLE, G. W.
 APPLICANT: WILSON, T. M.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inha AGENT
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

RESULT 7 ID US-08-241-766-14 STANDARD: PRT; 269 AA.
 XX AC xxxxxx
 DT DE XX
 XX DE XX
 Sequence 14, Application US/08241766
 CC Pat. No. 5686590
 GENERAL INFORMATION:
 APPLICANT: JACOBS, W. R.
 APPLICANT: COLLINS, D. M.
 APPLICANT: BANNERETTE, A.
 APPLICANT: DELISLE, G. W.
 APPLICANT: WILSON, T. M.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

RESULT 8 ID US-08-241-766-14 STANDARD: PRT; 269 AA.
 XX AC xxxxxx
 DT DE XX
 XX DE XX
 Sequence 14, Application US/08241766
 CC Pat. No. 5686590
 GENERAL INFORMATION:
 APPLICANT: JACOBS, W. R.
 APPLICANT: COLLINS, D. M.
 APPLICANT: BANNERETTE, A.
 APPLICANT: DELISLE, G. W.
 APPLICANT: WILSON, T. M.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/241,766
 FILING DATE: 12-MAY-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, GLADYS H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 22237-20003.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 CC SEQUENCE FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE: 269 AA: 28512 MW: 347982 CN:

Query Match 19.4%; Score 340; DB 1; Length 269;
 Best Local Similarity 33.1%; Pred. No. 2.04e-16;
 Matches 88; Conservative 66; Mismatches 93; Gaps 14;

5 DGDGRILVSYTITDSTIAFTIARYAQQVLT-GFDRLRL-TQRTDL-PAKAPL 61
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 4 LENKTYVIMGIANKRSTIAVGAKYLDQLGAKLVTVYRKERSKELEKQLNOPEAHLY 63
 Db 62 ELDYONEEHHLASLAGRVTETAGNKNKLGDGVHAI GEMPTQGMGINPFFDAPYADSKGIH 121
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 64 QIDQSDSEEVTINGFFQIGKVG -- N-IDGYYHSIAFANMEDL-RGRFSTS-SREGFLLAQD 119
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 122 ISAYSYASMKALLPIMMPSGSIYGMDF -DPSRAMPAYNMVMTYAKSALESVNREVARAG 180
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 120 ISSSSTLVIAHEAKKLMPMEGSIVATTYLGEGFAVONTNMVYAKASLEANVKYLALDIG 179
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 181 KYGVSNSLYAAGPRTLANSATYVGALGEAGAQIQLLEGNDRAPICWNMDATPVAK 240
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 180 PDNRIVNALSAAGPRTLSKAG-VGG-F-NT---I-LKEI-EERAPLKRNV-DQVEVGK 228
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 241 TVCAILSDWLPATPGDILYADGGAAHT 266
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 229 TAAYLLSDLSGVTGGENIHWDGFHA 254
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8 ID US-08-762-129-3 STANDARD; PRT; 244 AA.
 XX AC xxxxxx
 DE Sequence 3, Application US/08762129
 XX Sequence 3, Application US/08762129
 CC Patent No. 5756299
 GENERAL INFORMATION:
 CC APPLICANT: Hillman, Jennifer L.
 CC APPLICANT: Goli, Surya K.
 CC TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE
 CC NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
 CC STREET: 3174 Porter Drive

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/762,129
 FILING DATE: Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-835-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 IMMEDIATE SOURCE:
 TOPODY: Linear
 LIBRARY: GenBank
 CLONE: 416425
 SQ SEQUENCE: 244 AA: 25986 MW: 333095 CN;
 Query Match 12.8%; Score 224; DB 1; Length 244;
 Best Local Similarity 24.2%; Pred. No. 5.81e-08;
 Matches 44; Conservative 56; Mismatches 78; Indels 4; Gaps 3;
 Db 61 LGDMEATAEPALGGYGPVDLIVNNAYA-LMQPFELDTKEVDRSFVNLRSVQYQSIVYA 119
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 74 INGGFOIGDVGNDGVTHTIAFANMEDL-RGRFETS-SREGFLAQDISYSLTIVAKEAK 133
 Db 120 RSMIERGVRGSGIVNVSMVSHVTPGGLAISSTKGAMMLTKSNAMELGPHKTRVNSVNP 179
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 134 KLMP-E-G--GSIVATTYLGEGFAVONTNMVYAKASLEANVKYLALDGPDNLYNAIA 190
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 180 TVVLTAMGRSVTSDEPLARKLERHPMRFAEVEDVVSILFLSRSASTSGSSIFYDA 239
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 191 GPIRTLSAKVGEGENTILKEIEERAPLKRNVDOVEGKTAAYLSDSSGTGVIENHVDS 250
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 240 GY 241
 Qy 251 GF 252
 RESULT 9 ID US-08-762-129-4 STANDARD; PRT; 244 AA.
 XX AC xxxxxx
 DE Sequence 4, Application US/08762129
 XX Sequence 4, Application US/08762129
 CC Sequence 4, Application US/08762129
 CC Patent No. 5756299
 GENERAL INFORMATION:
 CC APPLICANT: Hillman, Jennifer L.
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: A NOVEL HUMAN CARBONYL REDUCTASE
 CC NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
 CC STREET: 3174 Porter Drive

ADDRESSSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 COUNTRY: CA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/762.129
 FILING DATE: Herevith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36.749
 REFERENCE/DOCKET NUMBER: PF-0171 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 LIBRARY: GenBank
 CLONE: 50004
 SEQUENCE: 244 AA; 25958 MW; 323866 CN;
 Query Match 12.5%; Score 219; DB 1;
 Best Local Similarity 25.3%; Prod. No. 1.12e-07
 Matches 46; Conservative 55; Mismatches 77
 61 LGDWDATERALGGIGPVLILVNAALYIMOFLEVTKEAFLITYSSSTKGAMTMLITI
 : ; : | : | : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 74 INGQEIQGDVGNDGIVHSTAFANMEDLRFGESEASREGF
 120 RDMINRGPGSIVNVNNSMVAHTFPNLITYSSSTKGAMTMLITI
 : ; : | : | : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 133 KKLMPEG--GSIVAVTYLGGEFAVQYINVMGAKASLEANVY
 180 TYYLTDMGKVSADPEFARKERPLRKFAEVEDVYNSLLE
 191 GPIRLSAKGVGFFNTLKEIERAPLURKRNVIDVEVGKTAAN
 240 GY 241
 : ;
 251 GF 252
 RESULT 10
 ID 08-762-129-1 STANDARD: PRT: 244 A
 XXXXXXXX
 Sequence 1, Application US/08/762.129
 Sequence 1, Application US/08/762.129
 Patent No. 5756299
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: A NOVEL HUMAN CARBONYL

CC APPLICANT: Bringer-Meyer, Stephanie
 CC APPLICANT: Sahn, Hermann
 CC APPLICANT: Hollenberg, Cornelies P
 CC TITLE OF INVENTION: MICROBIOLOGICAL METHOD OF MAKING
 CC NUMBER OF SEQUENCES: 7
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Firm of Karl F. Ross, PC
 CC STREET: 5676 Riverdale Ave.
 CC CITY: Bronx
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 10471-0500
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/594,808B
 CC FILING DATE: 07-FEB-1995
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Myers, Jonathan E
 CC REGISTRATION NUMBER: 26,963
 CC REFERENCE/DOCKET NUMBER: 19893
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (718) 884-6600
 CC TELEFAX: 718/601-1099
 CC TELEX: 620428
 CC INFORMATION FOR SEQ ID NO: 7:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 256 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE: 256 AA; 27256 MW; 327271 CN;

Query Match 9 8% Score 171; DB 1; Length 256;
 Best Local Similarity 24.0%; Pred. No. 2.99e-04;
 Matches 59; Conservative 74; Mismatches 100; Indels 13; Gaps 13;

Db 15 LVTGASRGICLTAKGLARYGAEVYLNGRNAMESLDSAQSCEEA-EGLKASTAEDVTDOD 73
 Qy 12 MGIAKNRSLAFGVAKYLDQGAKLVFTYKERSKELEKILEQNLNQEPAHLQYQDVSDE 71

Db 74 AVIDGVAATIERTDMGPIDILINNAGIQRRAFLLEE-FSRKDWD-LMSTNVA-YF-FVQQA 129
 Qy 72 EVINGEQIGKVGDGNIDGYHSIAFANMEDLRGRFSETSREGFLAQDISYSLTIVAE 131

Db 130 VARHMIPIRGKTYNCSYOSELARPGTAPYTAKGAVKNLTKGMDWGRHQGJQINGIA 189
 Qy 132 -AKKIMPEG GSIVATTYLGEEFAVQNTYMGVARAKSLEPNVYKTLALDQPDNTRVNAIS 189

Db 190 PGYFATEMTERIYAD-EEFTDWLCKRTPAGRWGQVEEL-VG-ARAVFLSSRASSEVNGOVL 246
 Qy 190 AGPITL-SAKGVGGFNTLKEITEERAPL-KRN-VDOVEVGKPAAYLLSDLSGGTGENI 246

Db 247 MVDGGI 252
 Qy 247 HVDSGF 252

RESULT 12
 ID US-08-375-962B-13 STANDARD; PRT: 244 AA.
 XX XXXXXX
 AC
 DT
 DE Sequence 13, Application US/08375962B
 XX Sequence 13, Application US/08375962B
 CC

Patent No. 5731195
 GENERAL INFORMATION:
 CC APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
 CC APPLICANT: CHRISTER, ERIKSSON, ULF
 CC TITLE OF INVENTION: Isolated Nucleic Acid Molecule
 CC Which Codes for A 32 kDa Protein Having 11-CIS Retinol
 CC Dehydrogenase Activity, and Which Associates With P63,
 CC a Portion of a Retinol Binding Protein Receptor
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Felife & Lynch
 CC STREET: 805 Third Avenue
 CC CITY: New York City
 CC STATE: New York
 CC ZIP: 10022
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 CC COMPUTER: IBM
 CC OPERATING SYSTEM: PC-DOS
 CC SOFTWARE: Wordperfect (ASCII standard)
 CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/375,962B
 CC FILING DATE: 20-January-1995
 CC CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/258,418
 CC FILING DATE: 6-October-1994
 ATTORNEY/AGENT INFORMATION:
 CC NAME: Pasqualini, Patricia A.
 CC REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
 TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (212) 688-9200
 CC TELEFAX: (212) 638-3884
 INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 244 amino acids
 CC TYPE: amino acid
 STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: E.coli 3-oxoacyl acyl carrier protein
 NAME/KEY: reductase (FABG)
 SEQUENCE: 244 AA; 25546 MW; 277421 CN;
 SQ

Query Match 9 4% Score 164; DB 1; Length 244;
 Best Local Similarity 22.4%; Pred. No. 9.02e-04;
 Matches 57; Conservative 76; Mismatches 110; Indels 12; Gaps 12;

Db 1 MNFEGKIALVYG-AS-RGIGRAETLAARGKVIGTATSENQAOISDYLG-A-N-GK- 55
 Qy 2 LNLENKYVIMGANKRSRAFGVAKVLDOLGAKLVFTYKERSKELEKILEQNLNQPEAH 61

Db 56 L-MLNVDPASIESVLEKIRAEFGEDVLDLYNNAGI-T-DNLMMMKDEFWND-LIETNL 112
 Qy 62 LYQIDVQSDEEVINGFEQIGKDVGNIDGYHSIAFANMEDLRGRFSETSREGFLAQDIS 121

Db 113 SVFRLSKAYTMRAMMKKRKG-RITITGSVYGTGMNGQQYAAKAGLIGFSKSLEARVAS 171
 Qy 122 S-YSLTVIAHEAKLMPMEGGSVIATTYLGEEFAVQNTYMGVARAKSLEPNVYKTLALDQGP 180

Db 172 RGITVNVVAPGFISTDMTRALSD-DQRA-GILAQPAGRGGAOEIANAVAFLASDEAAY 229
 Qy 181 DNTRVNAISAGPILRTLSAKGVGGFNTLKEITEERAPLKRNVNDQVEVGKPAAYLLSDLSGG 240
 Db 230 ITGETLHYNGMMV 244
 Qy 241 VTGENHVDSGFHAI 255

RESULT 13
 ID 5229279-7 STANDARD; PRT: 266 AA.

XX
AC xxxxxxxx
XX
XX 01-JAN-1900
DT
XX Patent No. 5229279.
XX
CC Patent No. 5229279
CC APPLICANT: PEOPLES, OLIVER P.; SUSKEY, ANTHONY J.
CC TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
CC BIOPOLYMERS
CC NUMBER OF SEQUENCES: 8
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/556,535
CC FILING DATE: 13 AUG 1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 67,695
CC FILING DATE: 29-AUG-1987
CC SEQ ID NO: 7
CC LENGTH: 246
SQ SEQUENCE 266 AA; 28572 MW; 399914 CN;

Query Match 8.1% Score 142; DB 3; Length 246;
Best Local Similarity 22.6%; Pred. No. 2.73e-02;
Matches 42; Conservative 60; Mismatches 74; Indels 10; Gaps 9;

Db 66 DSTKTAFKVKSVGEVDYLNNAGITRDRVFR-KMTRADWDA-VIDTNLTS--LFNVTK 121
QY 71 EEVINGFEQIGDVGNIIDGVYHSIAFANMEDURGRFSETSEGFLLAQDISSYSLTIVAH 130
Db 122 QVIDGMADRGWGRIVNLSVNSVQGQFGOTNVYSTAKAGLHGTMAQEAVFKGVNTV 181
QY 131 EAKLMP-E-G-SIVATVYLGEGFAVONYNNGVAKASLEANKYALDGDNIRVNAI 188
Db 182 SPGYIATDMKAIRQ-D-VLDKIVATPVKRGLPQ-EIASCAMLSESEESGSTGADES 238
QY 189 SAGPIRTLSAKGGFNTILKEIERAPLKR-NVDQVEVGKTAAYLLSDLSSGVTGENIH 247
Db 239 LNGGLH 244
Db 248 VDGFH 253
QY 248 VDGFH 253

RESULT 14
ID US-08-241-766-13 STANDARD; PRT; 247 AA.
XX
AC xxxxxxxx
XX DT
XX Sequence 13, Application US/08241766
CC Sequence 13, Application US/08241766
CC Patent No. 5686590
CC GENERAL INFORMATION:
CC APPLICANT: JACOBS, W. R.
CC APPLICANT: COLLINS, D. M.
CC APPLICANT: BANNERET, A.
CC APPLICANT: DELISLE, G. W.
CC APPLICANT: WILSON, T. M.
CC TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: MORRISON & FOERSTER
CC STREET: 755 Page Mill Road
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94304-1018
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,766
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE 247 AA; 2565 MW; 295036 CN;
SQ Query Match 6.7% Score 118; DB 1; Length 247;
Best Local Similarity 18.2%; Pred. No. 1.00e+00;
Matches 34; Conservative 60; Mismatches 87; Indels 6; Gaps 5;
Db 61 DVTDSDAVIDRAFTAVERHQGPVEVLVSAGLSA-DAFLMRTEKEKEF-KVNANLTG-
AF 117
QY 66 DVQSDEEVINGFEQISKDVGNIIDGVYHSIAFANMEDURGRFSETSEGFLLAQDISSYSL 125
Db 118 RVAQRARSMDRNKGMIIFGSVSSSGIGNQANVYASKVIGMARSTARELSKANVT 177
QY 126 TIVAEHKAKLMP-E-SIVATVYLGEGFAVONYNNGVAKASLEANKYALDGDNIRVNAI 184
Db 178 ANVVAQDIDDMTRALD-E-RIQQALQELPAKRYGTPAENAVGVSFLASEDASYLSGA 235
QY 185 VNAISAGPIRTLSAKGGFNTILKEIERAPLKR-NVDQVEVGKTAAYLLSDLSSGVTGENIH 247
Db 236 VLPVDGG 242
Db 245 NIHVDSG 251
QY 245 NIHVDSG 251

RESULT 15
ID US-08-137-175A-6 STANDARD; PRT; 299 AA.
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AC *****
XX DT
XX Sequence 6, Application US/08137175A
DE DE Sequence 6, Application US/08137175A
XX XX Sequence 6, Application US/08137175A
CC Sequence 6, Application US/08137175A
CC Patent No. 5777095
CC GENERAL INFORMATION:
CC APPLICANT: BARBOUR, Alan G.
CC APPLICANT: HANSSON, Lennart
CC APPLICANT: BANISTER, D. M.
CC APPLICANT: DELISLE, G. W.
CC APPLICANT: WILSON, T. M.
CC TITLE OF INVENTION: IMPROVEMENT IN BORRELLIA BURGDORFERI AND
NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BRODY AND NEIMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25

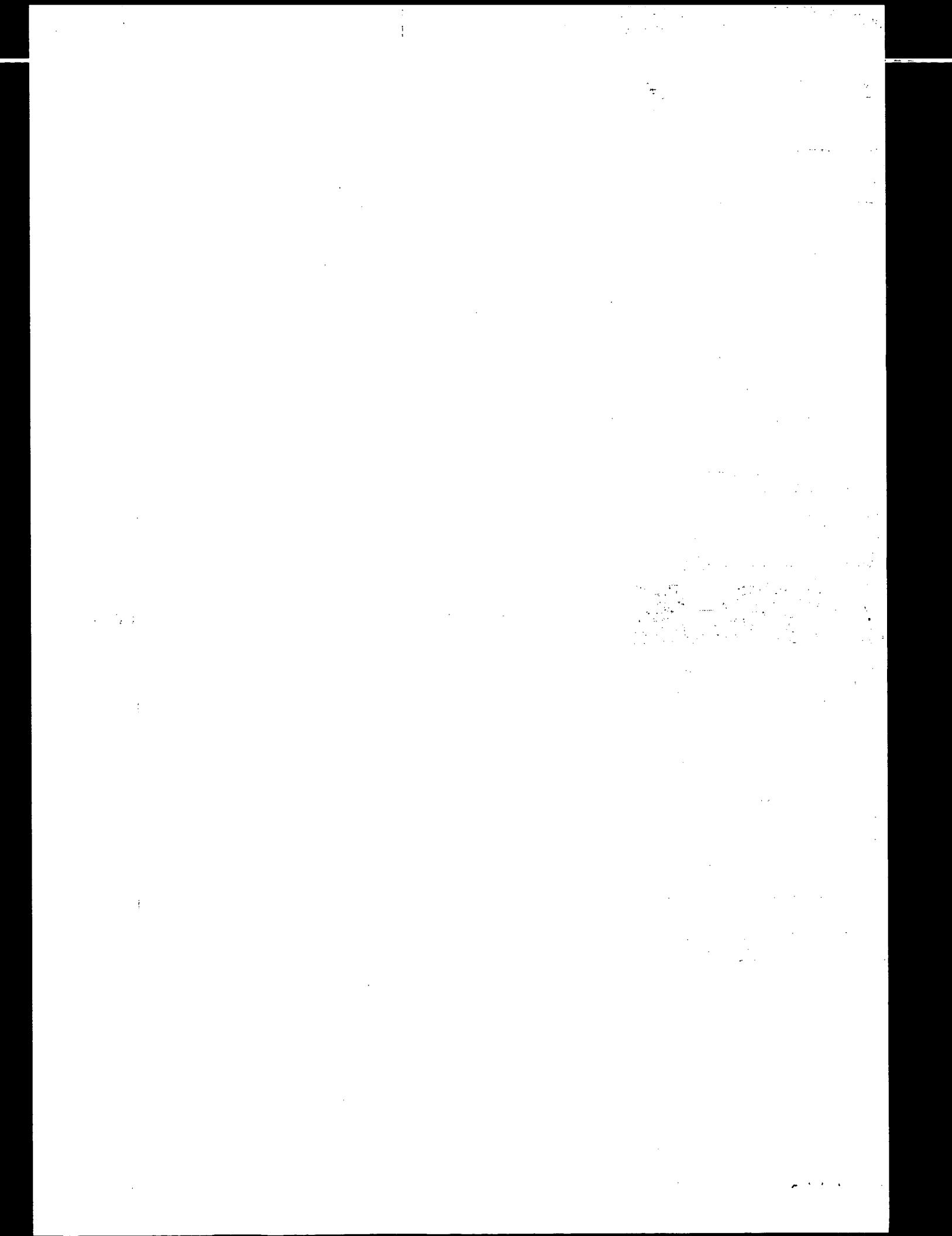
CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/1377-175A
 CC FILING DATE: 26-OCT-1993
 CC CLASSIFICATION: 424
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/08972
 CC FILING DATE: 22-OCT-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: COOPER, Iver P.
 CC REGISTRATION NUMBER: 28,005
 CC REFERENCE/DOCKET NUMBER: BARBOUR=1B
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-628-5197
 CC TELEFAX: 202-737-3528
 CC TELEX: 248633
 CC INFORMATION FOR SEQ ID NO: 6:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 299 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 SQ SEQUENCE 299 AA; 32432 MW; 487636 CN;

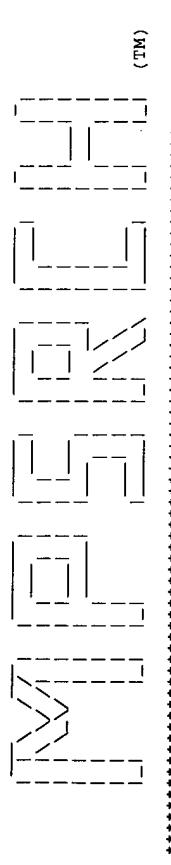
Query Match 6.3%; Score 111; DB 1; Length 299;
 Best Local Similarity 21.1%; Pred. No. 2.78e+00;

Matches 43; Conservative 59; Mismatches 89; Indels 13; Gaps 13;

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Qy	41	KEKRSKELEKLEQLNQEALKYQIDQSDEEVINGEQIGK-DVGNIDGYHSTIAFANM
Db	101	GKLEGTRADKTKVAMTIADDLNITIVTYDAASNKKTGSEVYRKGSV-IKESYKANLDS
Qy	100	EDURGRSESETSSREGFLAQDIISSYSLTIVAHAKKIMPEGGSGIVATYLGGEFAVONYV
Db	160	KKITREN-ETTLEYSEMTDSNDTKAVETLKGK-IK-LEGGSLYGG-KTTVKETEGTILT
Qy	160	MGVAKASLEANVKYLAIDLGPDRIR-YNAISAGPRTLSAKVGGFNTILKEIEERAPLK
Db	216	RELEQ-D-GKVKYL-NDTTSQST
Qy	219	RNYDQVEVGKTAAYLSDLSSGTT

Search completed: Fri Jan 15 15:04:49 1999
 Job time : 16 secs.





Release 3.1A John F. Collins, Biocomputing Research Unit.

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Distribution rights by Oxford Molecular Ltd

Mpsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jan 15 15:40:37 1999; MasPar time 43.45 Seconds
1102.362 Million cell updates/sec

Tabular output not generated.

Title: >US-08-790-043B-1
(1-771) from US08790043B.seq

Description: Perfect Score:
N.A. Sequence: Comp:

1 ATGCTTAATCTGAAACAA..... GATTCACCGCAATTAAATTAA 771

TACATTTAGAACTTTGT..... CTAAGGGCGTAAATTATT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 120476 seqs, 31064459 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-is-COMB 2:pct9_COMB 3:backfiles1

Statistics: Mean 8.068; Variance 4.336; scale 1.861

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
c 1	55	7.1	7218	1	US-08-232-	Sequence 14, Applicati
c 2	27	3.5	215	1	US-08-238-	1.62e-22 Sequence 5, Applicati
c 3	27	3.5	242	1	US-08-273-	3.01e-04 Sequence 1, Applicatio
c 4	24	3.1	215	1	US-08-238-	3.81e-04 Sequence 5, Applicatio
c 5	22	2.9	2894	1	US-08-472-	2.03e-02 Sequence 1, Applicatio
c 6	22	2.9	2894	1	US-08-472-	2.58e-01 Sequence 1, Applicatio
c 7	22	2.9	2894	1	US-08-483-	2.58e-01 Sequence 1, Applicatio
c 8	21	2.7	74	2	PCT-US95-1	8.05e-01 Sequence 100, Applicati
c 9	21	2.7	74	2	PCT-US95-1	8.05e-01 Sequence 94, Applicati
c 10	21	2.7	81	2	PCT-US95-1	8.05e-01 Sequence 98, Applicati
c 11	21	2.7	81	2	PCT-US95-1	8.05e-01 Sequence 92, Applicati
c 12	21	2.7	242	1	US-08-273-	8.05e-01 Sequence 1, Applicatio
c 13	21	2.7	774	2	PCT-US91-0	8.05e-01 Sequence 1, Applicatio
c 14	21	2.7	824	1	US-08-158-	8.05e-01 Sequence 1, Applicatio
c 15	20	2.6	42	1	US-08-452-	2.95e+00 Sequence 43, Applicati
c 16	20	2.6	54	1	US-08-452-	2.95e+00 Sequence 15, Applicati
c 17	20	2.6	54	1	US-08-452-	2.95e+00 Sequence 14, Applicati
c 18	20	2.6	75	2	PCT-US95-1	2.95e+00 Sequence 99, Applicati
c 19	20	2.6	81	2	PCT-US95-1	2.95e+00 Sequence 98, Applicati
c 20	20	2.6	82	2	PCT-US95-1	2.95e+00 Sequence 97, Applicati

ALIGNMENTS

RESULT 1
ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC xxxxxx

DT Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:

CC APPLICANT: DORNER, F.
CC APPLICANT: SCHEIFFINGER, F.
CC APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

CC COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: 26-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300 6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 883-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

RESULT 6
 ID US-0472-173-1 STANDARD; DNA; UNC; 2894 BP.
 AC xxxxxx

DT Sequence 1, Application US/08472173
 Sequence 1, Application US/08472173
 Patent No. 5655353

GENERAL INFORMATION:
 APPLICANT: LOOSMORE, Sheena M
 APPLICANT: YANG, Yan-Ping
 APPLICANT: CHONG, Peile
 APPLICANT: O'MEN, Raymond P.
 APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Activity

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472-173
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/472-173
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/296,149
 FILING DATE: 26-AUG-1994
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/296,149
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Stewart, Michael I.
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 STRANDEDNESS: single
 LENGTH: 2894 base pairs
 TYPE: nucleic acid

SEQUENCE 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 OTHER.

Query Match 2.9%; Score 22; DB 1; Length 2894;
 Best Local Similarity 75.0%; Pred. No. 2.58e-01;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2894 base pairs
 TYPE: nucleic acid

SEQUENCE 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 OTHER.

RESULT 7
 ID US-08-483-859-1 STANDARD; DNA; UNC; 2894 BP.
 AC xxxxxx

DT Sequence 1, Application US/08483859
 Sequence 1, Application US/08483859
 Patent No. 565436

GENERAL INFORMATION:
 APPLICANT: LOOSMORE, Sheena M.
 APPLICANT: YANG, Yan-Ping
 APPLICANT: CHONG, Peile

APPLICANT: O'MEN, Raymond P.
 APPLICANT: KLEIN, Michel H.
 TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Activity

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483-859
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/296, 149
 FILING DATE: 26-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/472-173
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/278, 091
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Stewart, Michael I.
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 OTHER.

Query Match 2.9%; Score 22; DB 1; Length 2894;
 Best Local Similarity 75.0%; Pred. No. 2.58e-01;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2894 base pairs
 TYPE: nucleic acid

SEQUENCE 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 OTHER.

RESULT 8
 ID PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
 AC xxxxxx

DT Sequence 100, Application PC/TUS9511934
 Sequence 100, Application PC/TUS9511934

GENERAL INFORMATION:
 APPLICANT: Cyrogen Corporation
 TITLE OF INVENTION: Antigen Binding Peptides (Abtides). From Peptide Libraries
 NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11934
 FILING DATE: 20-SEP-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrick, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-196-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER;
 Query Match 2.7%; Score 21; DB 2; Length 74;
 Best Local Similarity 4.8%; Pred. No. 8.85e-01;
 Matches 19; Mismatches 41; Indels 0; Gaps 0;
 Sequence 94, Application PC/TUS9511934
 GENERAL INFORMATION:
 APPLICANT: Cytogen Corporation
 TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From Peptide Libraries
 NUMBER OF SEQUENCES: 103
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11934
 FILING DATE: 20-SEP-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrick, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-196-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE 94 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER;
 Query Match 2.7%; Score 21; DB 2; Length 74;
 Best Local Similarity 4.8%; Pred. No. 8.85e-01;
 Matches 19; Mismatches 41; Indels 0; Gaps 0;
 Sequence 94, Application PC/TUS9511934
 GENERAL INFORMATION:
 APPLICANT: Cytogen Corporation
 TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From Peptide Libraries
 NUMBER OF SEQUENCES: 103
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11934
 FILING DATE: 20-SEP-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrick, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-196-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE 94 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER;
 Query Match 2.7%; Score 21; DB 2; Length 81;
 Best Local Similarity 4.8%; Pred. No. 8.85e-01;
 Matches 19; Mismatches 41; Indels 0; Gaps 0;
 Sequence 94, Application PC/TUS9511934
 GENERAL INFORMATION:
 APPLICANT: Cytogen Corporation
 TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From Peptide Libraries
 NUMBER OF SEQUENCES: 103
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11934
 FILING DATE: 20-SEP-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrick, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-196-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 base pairs

CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US91/05766.
 CC FILING DATE: 19910814
 CC CLASSIFICATION: 536
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/567,220
 CC FILING DATE: 14-AUG-1990
 CC ATTORNEY/AGENT INFORMATION:
 NAME: Lauver, Charlene A.
 CC REGISTRATION DOCKET NUMBER: D-5195 PCT
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (713)651-3634
 CC FAX: (713)651-5246
 CC INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 MOLECULE TYPE: unknown
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Gelonium multiflorum
 DEVELOPMENTAL STAGE: Seed
 TISSUE TYPE: Nut
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..774
 SEQUENCE 774 BP; 162 A; 64 C; 123 G; 102 T; 323 OTHER.

Query Match 2.7%; Score 21; DB 2; Length 774;
 Best Local Similarity 37.5%; Pred. No. 8.85e-01;
 Matches 18; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Db 542 ARAAYCARATHMGNAAYAATTCARCARMGNAATHMGNCNGCNAAYA 589
 Cp 486 AACACCCATCACATTAAATTTGAACCTGGATTGCACTTAAATA 439

RESULT 14
 ID US-08-158-353-1 STANDARD; DNA; UNC; 824 BP.
 AC xxxxxx
 DT Sequence 1, Application US/08158353
 CC Sequence 1, Application US/08158353
 CC Patent No. 5620862
 GENERAL INFORMATION:
 APPLICANT: Padula, Steven J.
 TITLE OF INVENTION: Methods for Diagnosing Early Lyme
 TITLE OF INVENTION: Disease
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/158, 353
 CC FILING DATE: 05-APR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/930, 600
 CC FILING DATE: 05-APR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US91/02362
 CC FILING DATE: 05-APR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/505, 314
 CC FILING DATE: 05-APR-1990
 CC ATTORNEY/AGENT INFORMATION:
 NAME: Brook Esq., David E.
 CC REGISTRATION NUMBER: 22,592
 CC REFERENCE/DOCKET NUMBER: RC90-01AZ
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (617) 861-6240
 CC FAX: (617) 861-9540
 CC INFORMATION FOR SEQ ID NO: 43:
 CC SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)
 SQ SEQUENCE 824 BP; 339 A; 104 C; 143 G; 238 T; 0 OTHER.
 Query Match 2.7%; Score 21; DB 1; Length 824;
 Best Local Similarity 83.9%; Pred. No. 8.85e-01;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 703 AAGAGCTGAAAAGTTATTGAAATCGATAAA 733
 Qy 137 AAGAGCTGAAAATTTAGAACATAAA 167

RESULT 15
 ID US-08-452-724A-43 STANDARD; DNA; UNC; 42 BP.
 AC xxxxxx
 DT Sequence 43, Application US/08452724A
 CC Sequence 43, Application US/08452724A
 CC Patent No. 5806550
 GENERAL INFORMATION:
 APPLICANT: Crea, Roberto
 TITLE OF INVENTION: Walk-Through Mutagenesis
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/452-724A
 CC FILING DATE: 30-MAY-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/930, 600
 CC FILING DATE: 05-APR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US91/02362
 CC FILING DATE: 05-APR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/505, 314
 CC FILING DATE: 05-APR-1990
 CC ATTORNEY/AGENT INFORMATION:
 NAME: Brook Esq., David E.
 CC REGISTRATION NUMBER: 22,592
 CC REFERENCE/DOCKET NUMBER: RC90-01AZ
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (617) 861-6240
 CC FAX: (617) 861-9540
 CC INFORMATION FOR SEQ ID NO: 43:
 CC SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: unknown
 SQ SEQUENCE 42 BP; 6 A; 3 C; 0 G; 8 T; 25 OTHER.
 Query Match 2.6%; Score 20; DB 1; Length 42;
 Best Local Similarity 23.8%; Pred. No. 2.95e+00;

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Page 3

Matches 10; Conservative 21; Mismatches 11; Indels 0; Gaps 0;
Db 1 SFTMACAKYATMMTMTSANYACMRCSTMNTSWTMAMSRT 42
Cp 265 ::::| |::| :|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:
CATCAATAATTGCCAACATCTTACCAATTGCTAAACCAT 224

Search completed: Fri Jan 15 15:41:24 1999
Job time : 47 secs.